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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/938,342

DATE: 09/18/2001
 TIME: 11:15:26

Input Set : A:\198069.txt
 Output Set: N:\CRF3\09182001\I938342.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
 5 (i) APPLICANT: Inze, Dirk
 6 Segers, Gerda
 7 De Veylder, Lieven
 8 Mironov, Vladimir
 10 (ii) TITLE OF INVENTION: METHOD AND MEANS FOR MODULATING
 11 PLANT CELL CYCLE PROTEINS AND THEIR USE IN PLANT
 12 CELL GROWTH AND CONTROL
 14 (iii) NUMBER OF SEQUENCES: 4
 C--> 16 (iv) CORRESPONDENCE ADDRESS:
 17 (A) ADDRESSEE: Nixon Peabody LLP
 18 (B) STREET: 990 Stewart Avenue
 19 (C) CITY: Garden City
 20 (D) STATE: New York, New York
 C--> 21 (F) ZIP: 11530
 23 (v) COMPUTER READABLE FORM:
 24 (A) MEDIUM TYPE: Floppy disk
 25 (B) COMPUTER: IBM PC compatible
 26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 29 (vi) CURRENT APPLICATION DATA:
 C--> 30 (A) APPLICATION NUMBER: US/09/938,342
 C--> 31 (B) FILING DATE: 24-Aug-2001
 32 (C) CLASSIFICATION:
 34 (vii) PRIOR APPLICATION DATA:
 35 (A) APPLICATION NUMBER: EP PCT/EP98/01522
 36 (B) FILING DATE: 13-MAR-1998
 37 (A) APPLICATION NUMBER: EP 97.200.765.2
 38 (B) FILING DATE: 14-MAR-1997
 40 (2) INFORMATION FOR SEQ ID NO: 1:
 42 (i) SEQUENCE CHARACTERISTICS:
 43 (A) LENGTH: 454 base pairs
 44 (B) TYPE: nucleic acid
 45 (C) STRANDEDNESS: double
 46 (D) TOPOLOGY: linear
 48 (ii) MOLECULE TYPE: cDNA
 50 (iii) HYPOTHETICAL: NO
 52 (vi) ORIGINAL SOURCE:
 53 (A) ORGANISM: Arabidopsis thaliana
 55 (ix) FEATURE:
 56 (A) NAME/KEY: CDS
 57 (B) LOCATION:15..276
 59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 61 CCTCTGAGAG AGAA ATG GGT CAG ATC CAA TAC TCC GAG AAA TAC TTC GAT 50
 62 Met Gly Gln Ile Gln Tyr Ser Glu Lys Tyr Phe Asp
 63 1 5 10

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65 GAC ACT TTC GAA TAC AGG CAC GTC GTT CTT CCT CCT GAA GTC GCT AAA      98
66 Asp Thr Phe Glu Tyr Arg His Val Val Leu Pro Pro Glu Val Ala Lys
67      15      20      25
69 CTT CTT CCA AAG AAT CGT CTT CTC TCC GAA AAC GAA TGG CGA GCG ATA      146
70 Leu Leu Pro Lys Asn Arg Leu Leu Ser Glu Asn Glu Trp Arg Ala Ile
71      30      35      40
73 GGA GTG CAG CAA AGC CGC GGA TGG GTA CAT TAC GCG GTT CAT CGA CCT      194
74 Gly Val Gln Gln Ser Arg Gly Trp Val His Tyr Ala Val His Arg Pro
75 45      50      55      60
77 GAG CCG CAC ATA ATG CTA TTC AGG AGG CCT CTT AAC TAT CAG CAG CAG      242
78 Glu Pro His Ile Met Leu Phe Arg Arg Pro Leu Asn Tyr Gln Gln Gln
79      65      70      75
81 CAG GAG AAT CAA GCT CAG AAC ATG CTT GTT AAG T GAATCATTAT      286
82 Gln Glu Asn Gln Ala Gln Asn Met Leu Val Lys
83      80      85
85 CATCACCTGA GTAAGAATGT TATATGCAAC AATTCTATGA GTATTGGTTT ATGTTTCTTG      346
87 TAAACATGGT TTGAATCTTT GTGGTTATGG ATGAATATGT GAGAGTTGGT TTGTTGAACA      406
89 ACTTCTATGT AATGTTAGTC TTGGTTCTAA TGTCATCTTC TGCTTCTC      454
92 (2) INFORMATION FOR SEQ ID NO: 2:
94 (i) SEQUENCE CHARACTERISTICS:
95 (A) LENGTH: 696 base pairs
96 (B) TYPE: nucleic acid
97 (C) STRANDEDNESS: double
98 (D) TOPOLOGY: linear
100 (ii) MOLECULE TYPE: DNA (genomic)
102 (iii) HYPOTHETICAL: NO
104 (vi) ORIGINAL SOURCE:
105 (A) ORGANISM: Arabidopsis thaliana
107 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
109 ATGGGTTCAGA TCCAATATC CGAGAAATAC TTCGATGACA CTTTCGAATA CAGGTAAAGC      60
111 TCTTCAATCT CGCTTCTTCT TCCTCCAATT TTCACTCTCA CTTCTCTAAT CGTAATCGAT      120
113 CGATACAGGC ACGTCGTTCT TCCTCCTGAA GTCGCTAAAC TTCTTCCAAA GAATCGTCTT      180
115 CTCTCCGAAG TAAGTTTTTT TCCGCATTGT TCTCTGATTT CTGATTCTAA ATCCTTCGAT      240
117 TAGATCATCG AAGACTATGA AAATTTGTTG CTCTTAAGAA ATTAAGTTTG GGAATAATCG      300
119 AAAAAGAGAT CGTTTAGGTT TAGGATTGTA ATCTTTGCTC TGAATCCAAA TTGCAACTGT      360
121 TACGATTTTG AATCTTTGCT TTGGGATTTT GTAAGGTTTA GTGATAAAGA GATTTTAGAC      420
123 ATTTGTGTTG TGCAATCTCT TCAATGTTGT ATTGATTGGT GGTGATGGTA AAAATGTTTG      480
125 GAATTTTCGAA GAACGAATGG CGAGCGATAG GAGTGCAGCA AAGCCGCGGA TGGGTACATT      540
127 ACGCGGTTCA TCGACCTGAG CCGCACATAA TGCTATTCAG GAGGCCTCTT AACTATCAGC      600
129 AGCAGCAGGA GAATCAAGCT CAGAACATGC TTGTAAAGTG AATCATTATC ATCACCTGAG      660
131 TAAGAATGTT ATATGCAACA GATCTATGAG TATTGG      696
133 (2) INFORMATION FOR SEQ ID NO: 3:
135 (i) SEQUENCE CHARACTERISTICS:
136 (A) LENGTH: 87 amino acids
137 (B) TYPE: amino acid
138 (C) STRANDEDNESS:
139 (D) TOPOLOGY: linear
141 (ii) MOLECULE TYPE: peptide
143 (vi) ORIGINAL SOURCE:

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144         (A) ORGANISM: Arabidopsis thaliana
146     (ix) FEATURE:
147         (A) NAME/KEY: Peptide
148         (B) LOCATION:1
150     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
152     Met Gly Gln Ile Gln Tyr Ser Glu Lys Tyr Phe Asp Asp Thr Phe Glu
153     1           5           10           15
155     Tyr Arg His Val Val Leu Pro Pro Glu Val Ala Lys Leu Leu Pro Lys
156           20           25           30
158     Asn Arg Leu Leu Ser Glu Asn Glu Trp Arg Ala Ile Gly Val Gln Gln
159           35           40           45
161     Ser Arg Gly Trp Val His Tyr Ala Val His Arg Pro Glu Pro His Ile
162           50           55           60
164     Met Leu Phe Arg Arg Pro Leu Asn Tyr Gln Gln Gln Glu Asn Gln
165           65           70           75           80
167     Ala Gln Asn Met Leu Val Lys
168           85
170 (2) INFORMATION FOR SEQ ID NO: 4:
172     (i) SEQUENCE CHARACTERISTICS:
173         (A) LENGTH: 72 amino acids
174         (B) TYPE: amino acid
175         (C) STRANDEDNESS:
176         (D) TOPOLOGY: linear
178     (ii) MOLECULE TYPE: peptide
180     (vi) ORIGINAL SOURCE:
181         (A) ORGANISM: Arabidopsis thaliana
183     (ix) FEATURE:
184         (A) NAME/KEY: Peptide
185         (B) LOCATION:1
187     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
189     Met Gly Gln Ile Gln Tyr Ser Glu Lys Tyr Phe Asp Asp Thr Phe Glu
190     1           5           10           15
192     Tyr Arg His Val Val Leu Pro Pro Glu Val Ala Lys Leu Leu Pro Lys
193           20           25           30
195     Asn Arg Leu Leu Ser Glu Asn Glu Trp Arg Ala Ile Gly Val Gln Gln
196           35           40           45
198     Ser Arg Gly Trp Val His Tyr Ala Val His Arg Pro Glu Pro His Ile
199           50           55           60
201     Met Leu Phe Arg Arg Pro Leu Asn
202     65           70

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VERIFICATION SUMMARY

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L:16 M:220 C: Keyword misspelled or invalid format, [(iv) CORRESPONDENCE ADDRESS:]
L:21 M:220 C: Keyword misspelled or invalid format, [(F) ZIP:]
L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]